



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/265,540A
Art Unit / Team No. : 1646
Date Processed by STIC: 6/9/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

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THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540A

DATE: 06/09/2000
TIME: 20:51:34

Input Set: I265540A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Parham, Christi L.
2 Moore, Kevin W.
3 Murgolo, Nicholas J.
4 Bazan, J. Fernando
5 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
6 <130> FILE REFERENCE: DX0804
7 <140> CURRENT APPLICATION NUMBER: US/09/265,540A
8 <141> CURRENT FILING DATE: 1999-03-08
9 <160> NUMBER OF SEQ ID NOS: 6
10 <170> SOFTWARE: PatentIn Ver. 2.0
11 <210> SEQ ID NO 1
12 <211> LENGTH: 1381
13 <212> TYPE: DNA
14 <213> ORGANISM: primate
15 <220> FEATURE:
16 <221> NAME/KEY: CDS
17 <222> LOCATION: (132)..(1064)
18 <220> FEATURE:
19 <221> NAME/KEY: misc_feature
20 <222> LOCATION: n at position 567 and 573
21 <223> OTHER INFORMATION: n may be A, C, T, or G; translated amino acid depends on g
22 <400> SEQUENCE: 1
23 tcgacccacg cgtccgcgct gcgactcaga cctcagctcc aacatatgca ttctgaagaa 60
24 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaaact 120
25 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
26 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr
27 1 5 10
28 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218
29 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
30 15 20 25
31 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266
32 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
33 30 35 40 45
34 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314
35 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
36 50 55 60
37 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362
38 Glu Thr Val Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
39 65 70 75
40 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410
41 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
42 80 85 90
43 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458
44 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr

P. 2
what about n's at locations
1336, 1342, 1369?

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Input Set: I265540A.RAW

45 95 100 105
46 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
47 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
48 110 115 120 125
49 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
50 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
51 130 135 140
52 **ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602**
53 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
54 145 150 155
55 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
56 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
57 160 165 170
58 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
59 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
60 175 180 185
61 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
62 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
63 190 195 200 205
64 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
65 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
66 210 215 220
67 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
68 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
69 225 230 235
70 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
71 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
72 240 245 250
73 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
74 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
75 255 260 265
76 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
77 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
78 270 275 280 285
79 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
80 Ser Cys Arg Arg Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
81 290 295 300
82 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
83 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
84 305 310
85 ggtgaagccg agaacctggt ctgcatgaca tggaaaccat gaggggacaa gttgtgtttc 1144
86 tgtttttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgct tacaagtcta 1204
87 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrggg 1264
88 gwtgtgacct ctgactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
89 **cttcacccct tgggtccaa gttttctcat ctgtaatggg ggatncctac aaaactg 1381**

90 <210> SEQ ID NO 2
91 <211> LENGTH: 311
92 <212> TYPE: PRT
93 <213> ORGANISM: primate
94 <220> FEATURE:

W-OK

W-->

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/265,540A

DATE: 06/09/2000
TIME: 20:51:34

Input Set: I265540A.RAW

95 <221> NAME/KEY: misc_feature / / / /
 96 <222> LOCATION: Xaa at residues 146, 148, 171, 214 and 225
 97 <223> OTHER INFORMATION: Xaa depends on corresponding codon
 98 <400> SEQUENCE: 2
 99 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
 100 1 5 10 15
 101 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
 102 20 25 30
 103 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 104 35 40 45
 105 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 106 50 55 60
 107 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 108 65 70 75 80
 109 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 110 85 90 95
 111 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 112 100 105 110
 113 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 114 115 120 125
 115 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 116 130 135 140
 W--> 117 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 118 145 150 155 160
 W--> 119 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
 120 165 170 175
 121 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 122 180 185 190
 123 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 124 195 200 205
 W--> 125 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 126 210 215 220
 W--> 127 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 128 225 230 235 240
 129 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 130 245 250 255
 131 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 132 260 265 270
 133 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 134 275 280 285
 135 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 136 290 295 300
 137 Leu Leu Arg Ala Trp Ile Ser
 138 305 310
 139 <210> SEQ ID NO 3
 140 <211> LENGTH: 1244
 141 <212> TYPE: DNA
 142 <213> ORGANISM: primate
 143 <220> FEATURE:
 144 <221> NAME/KEY: CDS

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TIME: 20:51:34

Input Set: I265540A.RAW

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145 <222> LOCATION: (2)..(694)
146 <400> SEQUENCE: 3
147 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49
148 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
149 1 5 10 15
150 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
151 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
152 20 25 30
153 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
154 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
155 35 40 45
156 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
157 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
158 50 55 60
159 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
160 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
161 65 70 75 80
162 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
163 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
164 85 90 95
165 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
166 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
167 100 105 110
168 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
169 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
170 115 120 125
171 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
172 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
173 130 135 140
174 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481
175 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
176 145 150 155 160
177 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529
178 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
179 165 170 175
180 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
181 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
182 180 185 190
183 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625
184 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
185 195 200 205
186 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
187 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
188 210 215 220
189 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggct ctgagccgag 724
190 Gln Asn Ser Gly Ala Val Cys
191 225 230
192 gaagctgctg atgtccatgt cagcacttta tggaatccgg tccctccattt tccgtgtcccc 784
193 aaaaggcccg tcagtgcctg tgaagatgta acgggtctca tgggggacgac aagcttattg 844
194 atttttttct tcaaactaag agtttttctaa tcatacgcggt ttttagaata attctacaga 904

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TIME: 20:51:34

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195      tatgtccccc aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgtaa 964
196      gcaaatgggc gtctggcacg cctctgacac tttttcgtca gcagccagga cacgagggtcc 1024
197      cctccttgat gaagcccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084
198      gacattaagt ggcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144
199      aatagtttca cagagattaa gccttttttt cccccaagtt aggaataaaa gactataaatt 1204
200      aactttttta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244
201      <210> SEQ ID NO 4
202      <211> LENGTH: 231
203      <212> TYPE: PRT
204      <213> ORGANISM: primate
205      <220> FEATURE:
206      <221> NAME/KEY: misc_feature
207      <222> LOCATION: Xaa at residue 64
208      <223> OTHER INFORMATION: Xaa translated amino acid depends on corresponding codon
209      <400> SEQUENCE: 4
210      Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
211      1 5 10 15
212      Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
213      20 25 30
214      Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
215      35 40 45
216      Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
217      50 55 60
218      Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
219      65 70 75 80
220      Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
221      85 90 95
222      Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
223      100 105 110
224      Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
225      115 120 125
226      Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
227      130 135 140
228      Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
229      145 150 155 160
230      Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
231      165 170 175
232      Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
233      180 185 190
234      Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
235      195 200 205
236      Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
237      210 215 220
238      Gln Asn Ser Gly Ala Val Cys
239      225 230
240      <210> SEQ ID NO 5
241      <211> LENGTH: 337
242      <212> TYPE: PRT
243      <213> ORGANISM: primate
244      <400> SEQUENCE: 5

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W-->O

Input Set: I265540A.RAW

| Line | ? Error/Warning | Original Text |
|------|---------------------------------------|---|
| 52 | W "N" or "Xaa" used: Feature required | ggg atg gag atc ncc aaa nat ggc ttc cac c |
| 89 | W "N" or "Xaa" used: Feature required | cttcatccct tnggtccnaa gttttctcat ctgtaatg |
| 117 | W "N" or "Xaa" used: Feature required | Ile Xaa Lys Xaa Gly Phe His Leu Val Ile G |
| 119 | W "N" or "Xaa" used: Feature required | Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp X |
| 125 | W "N" or "Xaa" used: Feature required | Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe S |
| 127 | W "N" or "Xaa" used: Feature required | Xaa Val Gln Gly Glu Ala Ile Pro Leu Val L |
| 216 | W "N" or "Xaa" used: Feature required | Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe G |

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821.825. Applicant's attention is directed to these regulations, published at 114 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123

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For PatentIn software help, call (703) 557-0400

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